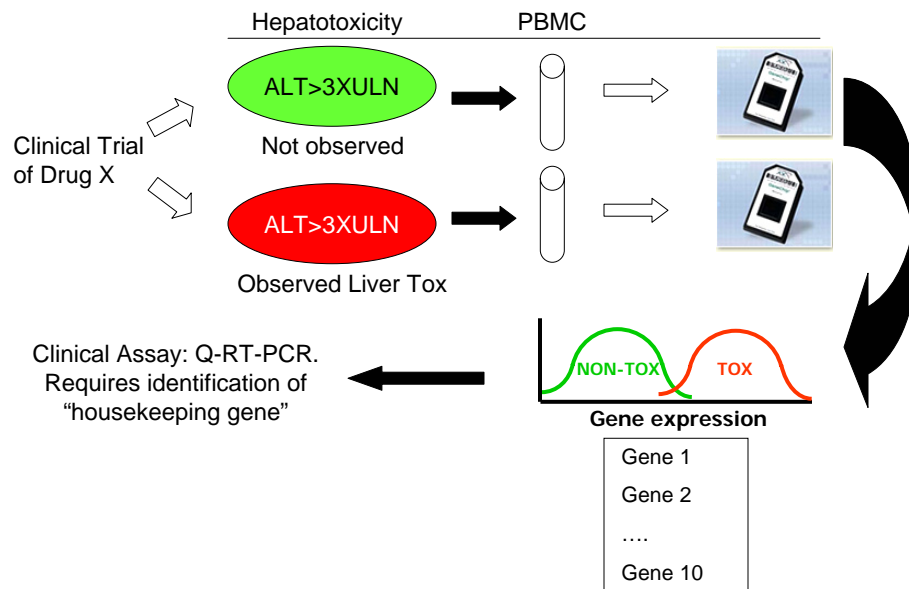
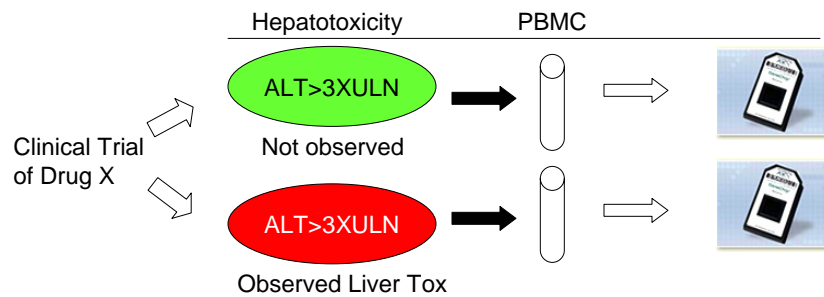


# **CASE STUDY : DEVELOPMENT OF CLINICAL HEPATOTOXICITY BIOMARKERS**

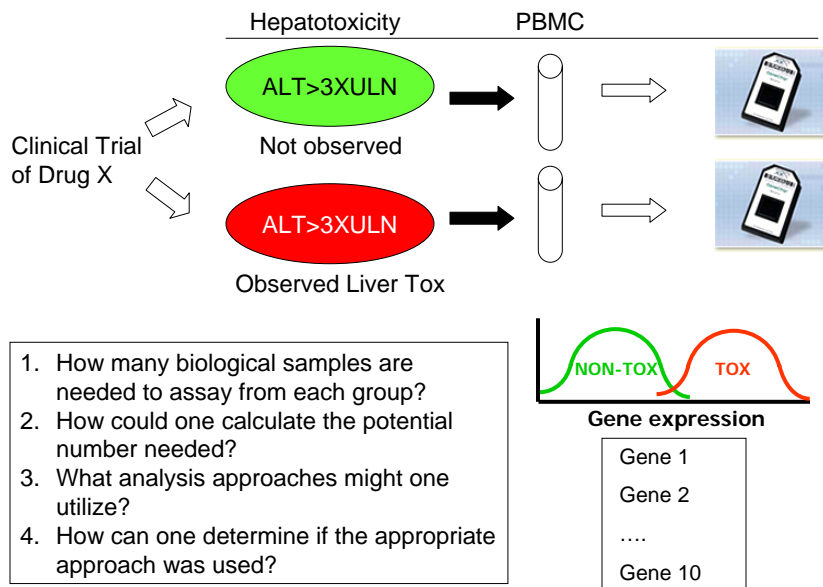


# **CASE STUDY : DEVELOPMENT OF CLINICAL HEPATOTOXICITY BIOMARKERS**



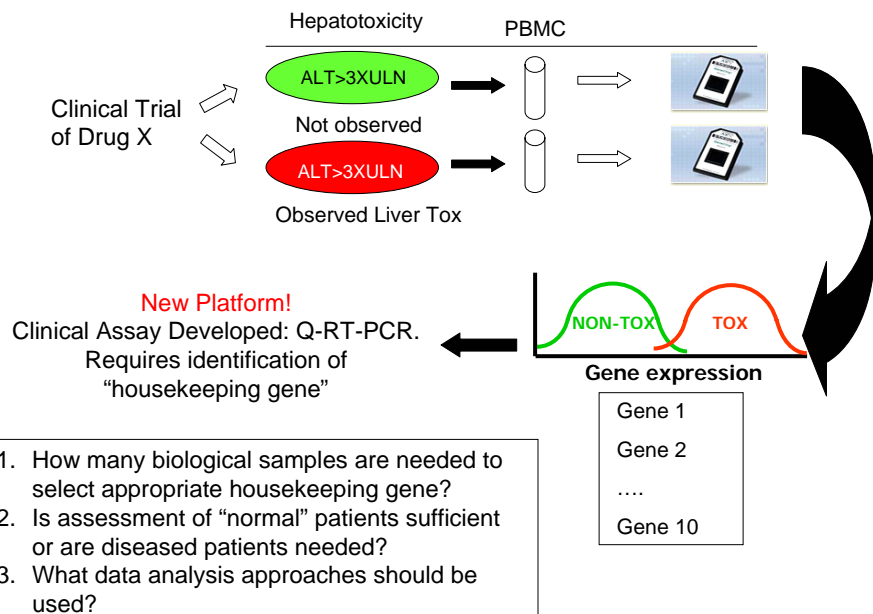
1. How many biological samples are needed to assay from each group?
2. How could one calculate the potential number needed?

### CASE STUDY : DEVELOPMENT OF CLINICAL HEPATOTOXICITY BIOMARKERS



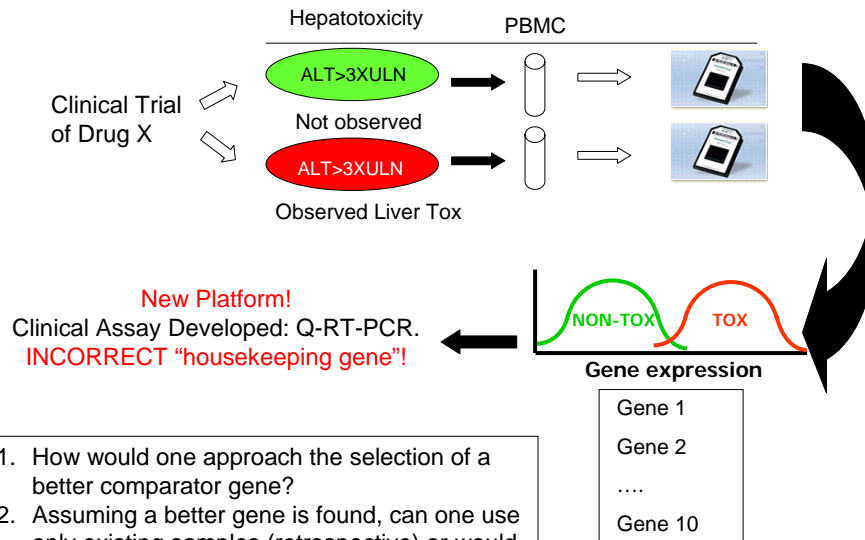
1. How many biological samples are needed to assay from each group?
2. How could one calculate the potential number needed?
3. What analysis approaches might one utilize?
4. How can one determine if the appropriate approach was used?

### CASE STUDY : DEVELOPMENT OF CLINICAL HEPATOTOXICITY BIOMARKERS



1. How many biological samples are needed to select appropriate housekeeping gene?
2. Is assessment of "normal" patients sufficient or are diseased patients needed?
3. What data analysis approaches should be used?

# CASE STUDY : DEVELOPMENT OF CLINICAL HEPATOTOXICITY BIOMARKERS



1. How would one approach the selection of a better comparator gene?
2. Assuming a better gene is found, can one use only existing samples (retrospective) or would new trial be needed?